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Result
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Listing first 45 summaries
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(c) 1993 - 2000 Com
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  XOPE_MOUSE
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118.689 Million cell updates/sec
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1563 AVKRLSTEKESEILQFNSRLADLEYHKSQVESELGRSKLKLASTTEELQLAENERLSLTT 1622

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1623 RMLDLQ 1628

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EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYEN----

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EDNQLATNKLKNQLDHLNQEIRLKEDVLKEKESLIISLEESLSNQRQKESSLLDAKNELE 1445

Query Match
Best Local Similarity 23.6
Matches 58; Conservative

16.0%; 23.6%;

; Score 170.5; DB 1; ; Pred. No. 0.027; 53; Mismatches 92;

Length Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 273:5385-5388(1998).

- PUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO THE TARREST MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANE IN PROXIMITY (BY SIMILARITY).

- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.

- DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.

- PTM: PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS. DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATION PROMOSTES DISSOCIATION.
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060763;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pl15 (Transcytosis protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sohda M., Misumi Y., Yano A., Takami N. "Phosphorylation of the vesicle docking association with the Golgi membrane.";
                                                                                                                                                                                                                                                                                       Phosphorylation.
                                                                                                                                                                                                                                                                                                     Transport;
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LEELRQQVSTLKCQNEQLQTAVTQQVSQIQQHKDQYNLLKIQLGKDNQHQGSYSEGAQMN 725
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                                                         IFDHEFTKLVKELEGVITKAIYKSSEEDKKEEEVKKTLEQHDN--IVTHYKNMIREQDLQ 665
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65; Conser
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n transport; Golgi stack;
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Pred. No. 0.01
52; Mismatches
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S->A: LOSS OF PHOSPHORYLATION
Z: 2E748F2C1BC2B942 CRC64;
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ASP/GLU-RICH (ACIDIC).
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Catarrhini; Hominidae;
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protein p115
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01-OCT-1989 (Rel. 1
16-OCT-2001 (Rel. 4
             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment I.;
                                                                                                                                                                 "X-ray structures of the myosin motor dom discoideum complexed with MgADP.BeFx and Biochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                     Wagle G., Noegel A., Scheel J., Gerisch "phosphorylation of threonine residues of Dictyostellum myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=95345067; PubMed=7619796;
                                                                                                                                                                                                                                                                                                                                                            "Replacement of threonine residues by phosphorylatable heavy chain fragment FEBS Lett. 269:239-243(1990).
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Lueck-Vielmeter D., Schleicher M., Grabatin B., Wippler J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-87092266; PubMed=3540939;
Warrick H.M., de Lozanne A., Lein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold) Eukaryota; Mycetozoa; Dictyosteliida;
                                                                Biochemistry
                                                                                      truncated head of Dictyostelium discoideum
                                                                                                                  Smith C.A., Rayment
                                                                                                                                                                                                                    Fisher A.J.,
                                                                                                                                                                                                                                 x-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=95345066; PubMed=7619795;
                                                                                                                                                                                                                                                                                                                      MEDLINE=88112226; PubMed=2828113;
                                                                                                                                                                                                                                                                                                                                                                                                    Gerisch G.;
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                                                                             resolution."
                                                                                                    "X-ray structure of the magnesium(II)-pyrophosphate
                                                                                                                                                                                                          Rayment I
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'X-ray structure of the magnesium(II).ADP.vanadate complex of the
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                                                                34:8973-8981(1995).
                                                                                                                                                                                                                    Smith C.A., Thoden
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R Pfam; PF02736; Myosin_head; 1.
R Pfam; PF02736; Myosin_N; 1.
R PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; Myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM000242.
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"X-ray crystal structure and solution fluorescence character
of Mg.2'(3')-0-(N-methylanthraniloy1) nucleotides bound to t
Dictyostellum discoideum myosin motor domain.";

J. Mol. Biol. 274:394-407(1997).

-1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS
ACTIVITY THAT IS ACTIVATED BY ACTIN.

-1- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-AS
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC),
LICHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN
                                                                                                                                                     InterPro;
Pfam; PF0
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or send an email to license@isb-sib.ch).
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"X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP of the Dictyostelium discoideum myosin motor domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum myosin motor domain to 1.9-A resolution."; Biochemistry 35:5404-5417(1996).
Myosin; Coiled coil; Actin-binding; ATP-binding; 3D-structure; Calmodulin-binding; Methylation; Alkylation; Phosphorylation.
                 SMART; SM00242; MYSC; 1
PROSITE; PS50096; IQ; 1
Myosin; Coiled coil; Act
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DictyDb; Db01008; mhcA.
InterPro; IPR000048; IQ.
InterPro; IPR0004009; Myosin_N.
InterPro; IPR001609; myosin_he
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S00250; S00250.
MMA; 03-DEC-97.
MMD; 17-AUG-96.
MMG; 03-DEC-97.
MMG; 03-DEC-97.
MMD; 17-AUG-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION (688).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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PTM: HOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.

MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1
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use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                  This
                                                                                                                                                        TISSUE=Tadpole head;
MEDLLNE=92398961; PubMed=1524825;
Hemmati-Brivanlou A., Mann R.W., Harland R.M.;
"A protein expressed in the growth cones of emneurons defines a new class of intermediate fi
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrach Xenopodinae; Xenopus.
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                                                       EMBL
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                                                                                                              SPINAL
                      for
           ch/announce/
                                  in
                                                       outstation
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Best Loc
Matches
                                             autoantigen.";
DNA Seq. 7:71-82(1997).

INA Seq. 7:71-82(1997).

PETROTION: MAY PLAY AN IMPORTANT ROLE IN SPER TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH DETECTABLE MALE ANTIGEN (SDM).

PETROTION OF THE SPECIFICITY: HIGHLY EXPRESSED IN TEST FOUND IN SPERMATICS DURING SPERMATOGENESIS.
                                                                                                                                                                                                                                                   G160_MOUSE STANDARD; PRT; 1325 AA P55937; P55937; Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) Golgin-160 (Male-enhanced antigen-2) (MEA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN
                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                           male-enhanced antigen-2 (Mea-2):
                                                                                                                                                           STRAIN=CD-1; TISSUE=Testis; MEDLINE=97217683; PubMed=90
                                                                                                                                        "Cloning a
                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                   NCBI_TaxID=10090
                                                                                                                                                                                                                                              GOLGA3 OR MÈA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M99387; AAA49966.1;
PIR; JH0720; JH0720.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                198
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                     LEYDIG CELLS, (
- SIMILARITY: HIC
- CAUTION: IT IS
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                                                                                                                                                                                                                                                                                                                                                                                ---RSKLQTVYSELDQAKLELKSAQKD-----LQSADKEIMSLKKKLTMLQ
                                                                                                                                                                                                                                                                                                                                                                                                     ELEDILRDHEEEKALMEE---EIASFSQRLENFRVAPVAFKPVEVDDYARKLSEIWQGAV
                                                                                                                                                                                                                                                                                                                                                                                                                      EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA--SGEVADKLRK--DLFSS--
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                                                                                                                                       and molecular
                                                                                                                                                 Sutou S.;
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157
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                               5, SPERMATOGONIA, OR SPERMATOCYTES HIGH, TO HUMAN GOLGIN-160.
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                     UNCERTAIN
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2 (Mea-2): a putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 163.5;
Pred. No. 0.05
51; Mismatches
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COIL 1A.
LINKER 1.
COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
                    WHETHER
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                                                                                                                                                                                                             Craniata; Vertebrata; Sciurognathi; Muridae;
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(MEA-2).
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e family of the
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                                                                                   SPERMATOGENESIS AND/OR WITH THE SEROLOGICALLY
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; Murinae; Mus
                     MET-30
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Golgi
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Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1193
                                                                     TISSUE-Adductor muscle;
MEDLINE-91088319; PubMed-2263488;
Nyitray L., Goodwin E.B., Szent-G
"Nucleotide sequence of full leng
                                                                                                                                                          Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.;
"Complete primary structure of a scallop striated muscle chain. Sequence comparison with other heavy chains reveal that might be critical for regulation.";
J. Biol. Chem. 266:18469-18476(1991).
                                                                                                                                                                                                                                                                                                                       01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, striated muscle.
Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
x-ray Crystallography (2.8 angstroms) of MEDLINE=94173332; PubMed=8127365;
                                                                                                                                                                                                                                  TISSUE=Adductor muscle; MEDLINE=92011595; PubMed=1917970;
                                                                                                                                                                                                                                                                                          Pectinoidea; Pectinidae; NCBI_TaxID=31199;
                                                                                                                                                                                                                                                                                                                                                                                                               MYS_AEQIR P24733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1026
                                           Nucleic
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatogenesis; Developmental protein. DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D78270; BAA19612.1; HSSP; P18852; 1SCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REHNSILETALAKREADLVQLNLQVQAVLQRKEEEDRQMKQLVQALQVSLEKEKMEVNSL
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                                           myosin
c Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
                                          heavy chain.";
Res. 18:7158-7158(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1SCG.
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%;
23.1%;
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                                                                        Szent-Gyorgyi
ıll length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 161; DB 1
Pred. No. 0.06;
48; Mismatches
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X
                                                                       length
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                                                                        scallop striated
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                                                                                                                                                                                                                                                                                                                           Pectinoida;
                                                                                                                                                                                                       myosin
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Matches 56
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between
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                                                                                                                                                                                  NP_BIND
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00063; myosin_head; 1. Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
    1055
                                                                                                                                            TURN
HELIX
                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) MEDLINE=96419133; PubMed=8805510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xie X., Harrison D.H., Schlichting I., Sweet R.M., Kalabokis V Szent-Gyorgyi A.G., Cohen C.; "Structure of the regulatory domain of scallop myosin at 2.8-A resolution.";
                                                                                                                    SEQUENCE
                                                                                                                                                                       HELIX
                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002017; Spectrin.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houdusse A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:306-312(1994)
                            10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MUSCLE CONTRACTION.

FUNCTION: MYSOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.

SUBUNIT: MUSCLE MYSOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S13557;
A40997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
DLKSTQENVEDLERVKRELEENVRRKEAEISSLNSKLEDEQNLVSQLQRKIKELQARIEE 1114
                         DLAQEEENVLDREFLKNEL-DNVR----AQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1WDC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X55714; CAA39247.1;
                                                                                                                                                                                                                                                                                                                 SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                             SM00015; IQ;
                                                     Similarity 28.
56; Conservative
                                                                                                                                                                                                                                                                                        Muscle
                                                                                                                                                                                                                                                                                                    PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 11-JUL-96.
IPR000048; IQ.
IPR004009; Myosin_N.
IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-94
                                                                                                                 778
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836
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                                                                                                                                                                                                                                                                          lkylation;
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28.1%;
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                                                                                                                                                                                                                                                            Coiled coil; Thick filament; Calmodulin-binding; 3D-struc MYOSIN HEAD-LIKE.
                                                     46;
                                                                                                                   MW.
                                                 Score 160.5;
Pred. No. 0.09
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain of
                                                                                                                                                                                                          RODLIKE TAIL (S2 AND COILED COIL (POTENTIA ATP (BY SIMILARITY).
                                                                                                                                                                                  ALKYLATION
ALKYLATION
                                                                                                                 A5CCE4127D1A4896
                                                                160.5; DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scallop myosin
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                                                                                                                                                                                (SH-1)
(SH-2)
                                                                                                                                                                                                                     (POTENTIAL).
                                                                            DB
                                                                                                                                                                                                                                                                        3D-structure
                                                    70;
                                                                                                                                                                                (BY
                                                                                                                 CRC64
                                                                                                                                                                                                                                  LMM DOMAINS)
                                                                           Length
                                                                                                                                                                                SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                     Actin-binding;
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                                                                            1938;
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                                                  Gaps
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RESULT 7
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Transport;
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DOMAIN
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                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1169
                                                                                                               EMBL; X54378; CAA38253.1; -. EMBL; L03188; AAB00143.1; -. EMBL; U53668; AAB66659.1; -.
                                                                                                                                                                entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                Bai Y., Symington L.S.;
Submitted (MAY-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1992
01-MAY-1992
                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Kendrick K.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hostetter M.K., Herman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE OF 782-1790 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A cytoskeleton-related gene, uso1,
protein transport in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakajima H., Hirata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USO1 OR INT1 OR YDL058W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intracellular
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01-MAY-1992 (Rel. 22,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell Biol. 113:245-260(1991).
                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH 1 MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL
                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                            OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN
                                                                                                                                                                                                                                                                                                                                                         COMPLEX
                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED
                                                                                                                                                                                                                                                                                                      DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE,
                                                                                                                                                                                                                                                                                                                   MEMBRANES. PROBABLY PRESENT ON ER AND THE GOLGI COMPLEX.
                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLEKDKKDLKREMDDLES 1230
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ta A., Ogawa Y.,
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Last annotation updat
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              ; Golgi stack; Cytoskeleton; GLOBULAR HEAD.
COILED COIL (POTENTIAL).
CHARGED (HYPER-HYDROPHILIC).
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Best Local :
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Q9UKX3; 095252;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
16-OCT-2001 (Rel. 40, Last annotation extrac
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                                       "The human extraocular muscle myosin heavy chain the cluster of fast and developmental myosin gene Genomics 54:188-189(1998).
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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   +
                                                                                    MEDLINE-99026150; PubMed-9806854;
Winters L.M., Briggs M.M., Schachat F.;
                                                                                                        TISSUE-Extraocular
                                                                                                                SEQUENCE OF 1917-1938 FROM N.A.
                                                                                                                                     Weiss A., Schiaffino S., Leinwand L.A.; "Comparative sequence analysis of the complete heavy chain family: implications for functional J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                              TISSUE-Extraocular muscle; MEDLINE-99318869; PubMed-10388558;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9606
                                                                                                                                                                                                                                                     Homo
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SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (NEARL) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
                                                                                                                                                                                                                                                    sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                              EKIRINAEENTVLKSKL
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DRHGNHVEG
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S (IN REF. 2).
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                                                              (MYH13) maps to chromosome 17.";
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InterPro;
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SMART; SM00242; MYSC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF111782; AAD29948.1; -. EMBL; AF075248; AAC83241.1; -. HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calmodulin-binding; ATP-binding; Methylation; Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02736; Myosin_N; 1. Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
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                                             158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES CHRACTERISTIC FOR ALPHA-HELICAL COLLED COLLS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLAMROUS: EACH MYOSIN HEAVY CHAIN CAN BE SELIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBERRAMENT (S2).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                    QEEENVL-----DREFLKNELDNVRAQLSQKDKEK-----RDSQVIIDTLRDTLEERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EW
European Bioinformatics Institute. There are no restr
KLDESQAELEAAQKESRSLSTELFKMRNAYEEVVDQLETLRRENKNLQEEISDLTEQIAE 1522
                                                                                          SKCASLEKTKQRLQG---EVEDLMRDL-----
                                                                                                               EAKAELQRALSKANSEVAQWKTKYETDAIQRTEELEEAKKKLAQRLQEAEEKTETA---N 1412
                                                                                                                                                                                                                               ATVVSLQQALGKAE--
                                                                                                                                                                                                                                                                            EEKESLISQLTKSKQALTQQLEELKRQMEEETKAKNAMAHALQSSRHDCDLLREQYEEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603487
                                          --EARKASGEVADK----LRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMS
                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non
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IPR004009; Myosin_N.
IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001609;
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843
179
659
761
130
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1938
186
681
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                                                                                                                                                                                                                                                                                                                                                                                       14.98;
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                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

MW: 1F6D006416381CD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>-</u>
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Pred. No. 0.11
8; Mismatches
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COILED COIL
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                                                                                       ERSHTACATLDKKQRNFDKVLAEWKQ
                                                                                                                                                                                                                                                                                                                                                                                       DB
.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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1523 TGKNL 1527

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RESULT
MYH7_RA
   EUR. HEART J. 5:181-121(15).

-!- FUNCTION: MUSCLE CONTRACTION.

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

-!- SUBUNIT: MUSCLE MYOSIN IS A HEXALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-!- SUBCELIULAR LOCATION: Thick fillaments of the myofibrils.

-!- SUBCELULAR LOCATION: THICK fillaments of the myofibrils.

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED CONLS.

-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

-!- MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYH7_RAT
P02564;
21-JUL-1986
01-OCT-1989
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete nucleotide sequence of full cardiac myosin heavy chain.";
             the Europuse by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                           -i-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McNally E.M., Kraft R., Bravo-Zehnder M., Taylor D., "Full-length rat alpha and beta cardiac myosin heavy Comparisons suggest a molecular basis for functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy MYH7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahdavi V., Periasamy M., Nadal-Ginard "Molecular characterization of two myos in the adult heart";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                          availability.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;
"Cardiac myosin heavy chain isozymic transitions during development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 297:659-664(1982).
[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90016823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=85179510; PubMed=6241892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1871-1935 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1524-1935 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Biol.
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s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comitties requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                               MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 SUBFRAGMENT (S2).

MISCELLANEOUS: THE CARDIAC ALPHA ISOFORM IS A 'FAST' MYOSIN, WHILE THE BETA ISOFORM IS A 'SLOW' ATPASE. SIMILARITY: CONTAINS 1 MYOSIN LIKE GLOBULAR HEAD DOMASIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         under pathological conditions are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0016823; PubMed=2798112;
Bravo-Zehnder M., Taylo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 01,
(Rel. 12,
(Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210:665-671(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Heart;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7045682;
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    Last sequence update)
    Last annotation update)
    cardiac muscle beta isoform

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.,
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 (See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor D., Leinwand L.A.; yosin heavy chain sequences functional differences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy
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MYSS_CYPCA
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Pfam; PF01576; Myosin_tail;
PRINTS; PR00193; MYOSINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000048; InterPro; IPR004009; InterPro; IPR002928;
                         MYSS_CYPCA
Q90339;
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                                                                             1361 LSKANSEVAQWRTKYETDAIQRTEELEEAKKKL--AQR-LQDAEEAVEAVNAKCSSLE
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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ATP-binding; Methylation;
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$02989; A
$02989;
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                                                                                              ADKLRKDLFSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                                                                                  KANLEKMCRTLEDQMNEHRSKAEETQRSVNDLTRQRAKLQTENGELSRQLDEKEALI-SQ 1300
                                                                                                                                                                                     AAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDDVTSNMEQ
                                                                                                                                                                                                                                         RTIINKLFFDLAQEEENVLDR---------
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J00752; AAA41654.1;
M32698; AAA41659.1;
                                                                                                                LTRGKLTYTQQLEDLKRQLEEEVKAKNALAHALQSARHDCDLLREQYEEETEAKAELQRV
                                                                                                                                  ĽΡ
                                                                                                                                                                  LGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; SM00015; IQ; 1.; SM00242; MYSC; TE; PS50096; IQ;
                                                                                                                                                                                                                                                          . Similarity 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      1784
1851
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Last sequence up
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coiled coil;
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ALKYLATION
IRK -> VRR
D -> + (IN
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' ' ' '
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Pred. No. 0.12;
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N (SH-2) (POTEN
R (IN REF. 3).
N REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  family;
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                                                                                                                                                             ----MEQIELLLQSQ 121
                                                                                                                                                                                                                                                                             1935;
                                                                                                                                                                                     ----IIKA 1241
                                                                                                                                                                                                                                                           ; 68
                                                                             1415
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update)

update)

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Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_v; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PF0DOM; PD000355; myosin_head; 1.
CMART. CWART. CMART. TO. 1
                                                                                                                                                                               EMBL; D50476;
EMBL; D43700;
HSSP; P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              different primary structures in carp fast skeletal muscle."; Biochem. Biophys. Res. Commun. 208:118-125(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural differences in the crossbridge head of "Structural differences in the crossbridge head of
                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe "cDNA cloning of myosin heavy chain isoforms from carp muscle and their gene expression associated with tempe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watabe S., Imai J., Nakaya M., Hirayama Y., Uozumi T., Hirono I., Aoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95194396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1387-1528 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acclimation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle."
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MEDLINE=97352533; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyprinus carpio
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                                                                                                                                                                InterPro; IPR000048; IQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exp. Biol.
                                                                                                                                                                                                                                                                                                                                                                        SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (1
                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.
                                                                                                                                                                                                                           D89992;
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Hirayama Y., Kikuchi K.,
                                                                                                                                                                                                                                                       requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle;
                                                                                                                                                                                            BAA22069.1; -. BAA09069.1; -. BAA07802.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Common carp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okamoto Y., Masaki
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Best Local S
Matches 57
                                                                                    Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases:

-: FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDP_MOUSE STANDARD; PRT; 941 AA. 992120; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) General vesicular transport factor pl15 (Transcytosis associated protein) (TAP) (Vesicle docking protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1409
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                                                                                                                                                                                                                                                                                                                    STRAIN-129;
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1238
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                         "Identification of mouse TAP (transcytosis associated protein/pll5).";
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BETWEEN THE CYTOSOL AND THE GOLGI APE
SIMILARITY).
DOMAIN: COMPOSED OF A GLOBULAR HEAD,
COIL) AND A HIGHLY ACIDIC C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSKCASLEKTKQRLQ
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57; Conserv
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29; TISSUE=Thymus;
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Pred. No. 0.14
51; Mismatches
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ACTIN-BINDING.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (TRI-) (PO ALKYLATION (SH-1). ALKYLATION (SH-2). MW; 9A1244B67D63C83B C
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                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                      DURING
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AN ELONGATED DOMAIN.

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Best Local :
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                           Eukaryota; Merachia;
Amphibia; Batrachia;
.....nodinae; Xenopus.
                                                                                                                                                                                                   P50533;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
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                                                                                                                          Xenopus laevis (African clawed frog)
                                                                                                                                                      XCAP-E
                                                                                                                                                                          Chromosome assembly protein
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InterPro; IPR000219; RhoGEF.
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                   Xenopodinae; Xe
NCBI_TaxID=8355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER; PHOSPHORYLATED IN INTERPHASE BUT MITOTIC CELLS. DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATION PROMOSTES DISSCCIATION (BY SIMILARITY). SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1929095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----VSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLEL
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                                                                                                                                                                                                                                                                                                                STANDARD;
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912
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                                                                                            Chordata;
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                                                                     Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                   a; Craniata; Vej
Mesobatrachia;
                                                                                                                                                                               XCAP-E.
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2; Mismatches
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COILED COIL (POTENTIAL).
ASP/GLU RICH (ACIDIC).
PHOSPHORYLATION (BY SIMILARITY).
R; AB5C10895CD7E508 CRC64;
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                                                                                                                                                                                                                               update)
                                                                                            Vertebrata; Euteleostomi;
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                                                                   Pipoidea;
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Best Local
16 'Uli'-2007.
Myosin heavy chain, skeletal muserr,
Myosin heavy chain, skeletal muserr,
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; "Leeise Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                      MYH4_RABIT STANDARD; PRT; 19
(2864);
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
SEQUENCE
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use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MITOTIC CHROMOSOMES.

-:- SUBUNIT: ASSOCIATES WITH XCAP-C PROBABLY AS HETERODIMER.

-:- SUBCELLULAR LOCATION: NUCLEAR, DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E MAS RECRUITED TO THE CHROMOTIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.

-:- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.

-:- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 79:449-458(1994).
-!- FUNCTION: REQUIRED FOR BOTH ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U13674; AAA64680.1; -. HSSP; P07751; 1AJ3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        condensation in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02483; SMC_C; 1. Pfam; PF02463; SMC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95042742; PubMed=7954811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A heterodimeric coiled-coil protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
KAQDELAKQKEIIMGHDKEIKTKSSEAGKLRENNNDLQ
                                           TVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                       LELEELKREO
                                                                                                                                 PEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQ
                                                                                                                                                                               EVQKKAEEKFKVLEHKMKNAEAERERELKEAQQKLDTAKKKADASNKKMKEKQQEVDALV
                                                                                                                                                                                                                      QALGKAEMLCSTLKKQMKYLEQQQD-ETKQAQEEAGRLRSKM----KTMEQIELLLQSQL 122
                                                                                                                                                                                                                                                                    KNTVERYRQLKQQWEMKSEEAELLQTKLQQSSYHKQQEE--LDSLKQTIEESEETLKNTK 764
                                                                                                                                                                                                                                                                                                                ENVLDR-----EFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQ
                                                                                                                                                                                                                                                                                                                                                            l Similarity
48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
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ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
ALA/ASP-RICH (DA-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                          Score 155.5; D
Pred. No. 0.11;
4; Mismatches
                                                                                       TTYKQQIETVDEAMKAYQEQADSMASEVSKNKEAVK
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                           220
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                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                   PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                              Calmodulin-binding;
                                                                                                                                                                                                                                                                        Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                    PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32574; AAA74199.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal muscle; Maeda K., Hostinova E., Roesch-Kleinkauf A., Schuster H.,
                                                                                                                                                                                                                                                     Multigene
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wittinghofer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal muscle and a novel cosynthesis of S-1 fragment with assential and regulatory light chains.";
              24 LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
 LGEQIDNLQRVKQKLEKEKSELKMEIDDLASNME---
                                                                                                                                                                                                                                                                                                                                                                                                                                  P08799;
                                                       Similarity
                                                                                                                                                                                                                                                     family
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179
658
760
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130
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756
                                            Conservative
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1938
1938
186
680
774
35
130
552
756
                                                       14.5%;
                                                                                                    223064
                                                                                                                                                                                                                                                                         Coiled
                                            49;
                                                                                                          MYOSIN HEAD-LIKE.

1Q.

COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (MONO-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

METHYLATION (TRI-) (BY SIMILARITY).

ALKYLATION (SH-1) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).

ALKYLATION (SH-2) (BY SIMILARITY).
                                                                                                   WW;
                                          Score 155; DE
Pred. No. 0.19
9; Mismatches
                                                                                                                                                                                                                                                                        coil; Thick filament; Actin-binding,
                                                                                                   D8A8A2EC5B182626 CRC64;
                                                                                                                                                                                                                                                             Methylation; Alkylation;
                                                      DB
19;
                                           ; 08
TVSKAKGNLEKMCRTLEDQ 1258
                                                                  Length 1938
                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gasperik J.,
                                            44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYH3_RAT
                                                                                                                                                                                                                                                                                                                                          AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR;
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYH3_RAT 
P12847;
                                                                                                                                                                                       EMBL; X04267; CAA27817.1;
                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1319
                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete nucleotide and encoded amino myosin heavy chain gene. Evidence again
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strehler E.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87060988; PubMed=3783701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomı;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1259
                                                                                                                          InterPro;
                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nadal-Ginard B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
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                                                                                                                                                                        A24922; A24922.
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                                                                                                                                                         P08799; 1MND
                                                                       IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR002017; Spectrin.
IPR001609; myosin_head.
                                                                                                                                         IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain, fast skeletal muscle, embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strehler-Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.

PR00193;

Pfam; PF00612; IQ;

InterPro;

InterPro;

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Best Local S
Matches 53
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P49454; 013246; 013171;

01-FEB-1996 (Rel. 33, Create

01-FEB-1996 (Rel. 33, Last s

16-OCT-2001 (Rel. 40, Last a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom;
SMART; S
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MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                           TISSUE-Breast carcinoma;

MEDILNE-95348175; PubMed-7542657;

Liao H., Winkfein R.J., Mack G., Rattner J.B., Y

"CENP-F is a protein of the nuclear matrix that
kinetochores at late G2 and is rapidly degraded
J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                      zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., C
Jones D., Yang-Feng T.L., Lee W.-H.;
"Characterization of a novel 350-kilodalton nuc
that is specifically involved in mitotic-phase
Mol. Cell. Biol. 15:5017-5029(1995).
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                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENPF.
  SEQUENCE OF 2194-3210 MEDLINE-95336446; Publ
                                                                                                                                                         MEDLINE-95379848;
                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE-Breast carc
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l Similarity 23.8%;
53; Conservative
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annotation update)
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Pred. No. 0.19
51; Mismatches
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ACTIN-BINDING.
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ALKYLATION (SH-1).
ALKYLATION (SH-2).
M; B5D546A596E5A696 CRC64;
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Query Match Best Local Matches

Local

Similarity 57; Conser

Conservative

55;

Mismatches

90;

Indels

40;

Gaps

7;

14.5%;

Score 155; DB Pred. No. 0.31;

Length 3210;

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CHARACTERIZATION.
MEDLINE-96437347; PubMed-9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
"Characterization of the kinetochore binding domain of CEN interactions with the kinetochore proteins CENP-F and hBUB J. Cell Biol. 143:49-63(1998).

-i-FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION,
                                                            CONFLICT
CONFLICT
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or send a
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"A novel cell-cycle-dependent 350-kba nuclear protein:
domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., "The C terminus of mitosin is essential for its nuclear centromere/kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                         REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95370296; PubMed=7642639; Zhu X., Chang K.-H., He D., Mancini
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                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH RETINOBLASTOMA PROTEIN (RB), CEND-E AND BUBRI. SUBUNIT: HOMO- OR HETERODIMER. SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN THE N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT N SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT N SUBCELLULAR LOCATION: NUCLEAR LOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; U19769; AAA82889.1;
; U30872; AAA82935.1;
; U25725; AAA86889.1;
; P02649; 1LE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pll5 (Tran
protein) (TAP) (Vesicle docking protein).
VDP.
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P41542;
01-NOV-1995
01-NOV-1995
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"pl15 is a general vesicular transport factor related to endoplasmic reticulum to Golgi transport factor Usolp.";
Proc. Natl. Acad. Sci. U.S.A. 92:522-526(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Transcytosis-associated protein (TAP)/pl15 is a general fusion factor required for binding of vesicles to acceptor membranes.", Proc. Natl. Acad. Sci. U.S.A. 92:527-531(1995).
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                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE. DOMAIN: COMPOSED OF A GLOBULAR HEAD, AN ELONGATED TAIL (COILED-COIL) AND A HIGHLY ACIDIC C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: GENERAL VESTCULAR TRANSPORT FACTOR REQUIRED FOR INTERCISTERNAL TRANSPORT IN THE GOLGI STACK, IT IS REQUIRED FO TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR AND TARGET MEMBRANES IN PROXIMITY.
                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER WITH TWO N-TERMINAL HEADS COILED-COIL TAIL. DIMER FORMED BY PARALLEL AS
                               European Bioinformatics Institute.
                                                                                                                                            SIMILARITY:
                                                                                                                                                                   DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE; PHOSPHORYLATION PROMOSTES DISSOCIATION (BY SIMILARITY).
                                                                                                                                                                                                                                                    PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER
                                                                                                                                                                                                                       PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS
                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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16-OCT-2001
                                                                                                                   Hammer J.A. III, Bowers B., Paterson B.M., Korn E.D.; "Complete nucleotide sequence and deduced polypeptide sequence nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of the complex of the 
                                                                                                                                                                                                                                       Eukaryota; Acanthamoebidae; Acanthamoeba
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InterPro; IPR001609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048;
            148
                                                                                954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e by non-profit institutions as long dified and this statement is not removed. titles requires a license agreement (See send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

(MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC OF ALPHA-HELICAL STRUCTURES. THIS REGION IS INTERRUPTED BY A HINGE AND JOINED BY A NONHELICAL TAILFIECE WHERE THE REGULATORY PHOSPHORYLATION SITES RESIDE.

MISCELLANEOUS: THE HINGE REGION MAY PLAY A KEY ROLE IN MEDIATING THE EFFECT OF HEAVY CHAIN PHOSPHORYLATION ON ENZYMATIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 2 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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           SLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQ--
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                                  ETKDALADAENISETLRSKLKNTERGADDVRNELDDVTATKLQLEKTKKSLEEELAQTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                          Coiled coil; Actin-binding; ATP-binding; Calmodulin-binding; tion; Alkylation; Phosphorylation; Multigene family.

1 789 MYOSIN HEAD-LIKE.
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ACTIN-BINDING.
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                                                                                                                                                                                      Score 154.5; I
Pred. No. 0.15;
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ALPHA-HELICAL TAILPIECE (LMM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myosin heavy chains they express.",

J. MUSCIE Res. Cell Motll. 16:35-43(1995).

-i- FUNCTION: MUSCLE CONTRACTION.

-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

-i- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

-i- SUBURIT: MUSCLE MYOSIN IS A HEXAMIL LIGHT CHAIN SUBUNITS (MLC.)

AND 2 RESULATORY LIGHT CHAIN SUBUNITS (MLC-2).

-i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

-i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, adult 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1130
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                        modified and this statement entities requires a license
                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Type IIx myosin heavy chain transcripts fibers of human skeletal muscle."; Am. J. Physiol. 267:C1723-C1728(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95109625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain family: implications for functional diversity.";
J. Mol. Biol. 290:61-75(1999).
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MEDLINE=99318869; PubMe
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                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ennion S., Sant'ana Pereira J., Sargeant T., Young A., Goldspink G., ^{\circ}Characterization of human skeletal muscle fibres according to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95270723; PubMed=7751403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schiaffino S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weiss A., Schiaffino S., Leinwand L.A.; "Comparative sequence analysis of the complete human sarcomeric myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                             SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE
SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                             PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 L
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SH
                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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AF111784; AAD29950.1; S73840; AAC13916.1; -
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this statement is not removed. U
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Q08378;

Q1-NOV-1997 (Rel. 35, 1

Q1-NOV-1997 (Rel. 35, 1

16-OCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
CONFLICT
SEQUENCE
                                                                                                             MEDLINE=93301617; PubMed=8315394; Fritzler M.J., Hamel J.C., Ochs R.L., Chan E.K.L.; "Molecular characterization of two human autoantigens: encoding 95- and 160-kD proteins of a putative family i
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                            Golgin-160 (Fragment).
GOLGA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1378
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SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                               complex.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
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ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
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Exp. Med. 178:49-62(1993).

- FUNCTION: GOLGI AUTO-ANTIGEN; MAY HAVE A FUNCTION I PROCESSING AND TRANSPORT OF PROTEINS THROUGH THE GO SIMILARITY: HIGH, TO MOUSE MALE-ENHANCED ANTIGEN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232858;
; P08799;
160740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSELKSKEEEQQRLINDLTAQRGRLQTESGEFSRQLDEKEALVSQLSRGKQAFTQQIEEL
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                                                                                                                                                                                                                                                                                                           Primates;
                                                                                                                                                                                                                                                                                                                              Chordata;
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23.3%;
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Last annotation updat
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Pred. No. 0.21
51; Mismatches
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K -> R (IN REF. 3)

MW; 681E866F83AEA8
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COILED COIL (POTENTIAL)
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                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; I Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681E866F83AEA83F CRC64
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Golgi
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                MEDLINE-90001496; PubMed-2362820;
Liew C.-C., Sole M.J., Yamauchi-Takihara K.,
Anderson D.H., Lin L., Liew J.;
                                                                                                                                                                  Pfordt M., Bach A., Vosberg H.P.;
"The complete sequence of the human beta-myosin heavy chain
a comparative analysis of its product.";
Genomics 8:194-206(1990).
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                               MYH7_HUMAN STANDARD; PRT; 1935 AA.
P12883; Q14904; Q16579;
01-OCT-1989 (Rel. 12, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, cardiac muscle beta isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-91065634; PubMed=2249844;
Jaenicke T., Diederich K.W., Haas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See
              MEDLINE=89264452;
Yamauchi-Takihara
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L06148; AAA35921.1; HSSP; P80220; IDIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                       SEQUENCE OF 1-115
                                                                Nucleic
                                                                            "Complete sequence and organization of heavy chain gene.";
                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                        MYH7 OR MYHCB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Golgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEQVAAAKVEAGHNRRHFKAASLELSEVKKELQAKEHLVQKLQAEADDLQIREGKHSQEI
                                                           chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 25.(
55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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579
66350 Þ
  PubMed=2726733;
K., Sole M.J., Li
of human cardiac
                                       FROM N.A
                                                               18:3647-3651(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                   Haas W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DEQLSKQPVGNQEMENLKWEVDQKEREIQSLKQQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 152.5; DE Pred. No. 0.075;
                                                                                                                                                                                                                                                                                  Catarrhini;
                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8C9A5A73D0128AEE CRC64;
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Liew J.,
ac myosin
                                                                                                                                                                                                                    Schleich
                                                                                        the
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  Ing D., Liew
heavy chain
                                                                                                                                                                                                                                                                                 Hominidae;
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                                                                                                                  Kellam
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                                                                                                                                                                                                                                                                                                                                  (MyHC-beta)
                                                                                         cardiac
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                                                                                                                                    VARIANT CMH1 GLN-403.
MEDLINE=90367131; Pub
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Am. J. Med. (
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Genet. 58:267-276(1995).
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MEDLINE-93343938; Pul
Harada H., Kimura A.,
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MEDLINE=92346810; Publ
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eve G., Thierfelder L., Watkins
Shono H., Nakao S., Tanaka H.,
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MEDLINE-89384556; PubMed=250643-,
A George E.L., Ober M.B., Emerson C.P. Jr.;
A "Functional domains of the Drosophila melanogaste heavy-chain gene are encoded by alternatively spin heavy-chain generatively spin heav
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WEDLINE-96209901; PubMed-8655135;

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KNAME C.-W., Lien W.-P., Liew C.-C.;

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01-JUN-1994 (Rel.
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"A high risk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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      Kronert W.A.,
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      O'Donnell P.T.,
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      STETT TTTT TO THE TRANCE OF THE PROPERTY OF TH
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   DOMAIN
NP_BIND
VARSPLIC
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00063; myosin_head; 7.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - I SUBUNIT: MUSCULE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

- I SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

- I ALTERNATIVE PRODUCTS: AS DROSOPHILA HAS A SINGLE MUSCLE MHC GENE, MHC ISOFORMS MUST RELY ON ALTERNATIVE RNA SPLICING THAT LEADS TO DIFFERENCES IN THE C-TERMINUS OF THE VARIOUS MHC PROTEINS.

- I MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

- I SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
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gene. Alternatively spliced transcripts
                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed.
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FUNCTION: MUSCLE CONTR
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                                                                                                                                                                                                                                                                                                                                                                   ; SM00015; IQ; 1.
; SM00242; MYSC; 1
TE; PS50096; IQ; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262:10741-10747(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mhc
                                                                                                                                                                                                                                                                                                                                 Coiled coil; Thick filament; Actin-binding,
MYOSIN HEAD-LIKE.

1Q.

COLLED COIL (POTENTIAL).
ATP (BY SIMILARITY).
P -> I (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
EK -> RE (IN REF. 2).
MW; 8C4FEC1BB8D310A9 CRC64;
          ¥
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                                                                                                                                                                                                                                                                                                   Alternative splicing;
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Usage

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RESULT
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             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                           protein
Plant P
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. SR1; TISSUE-Leaf;
MEDLINE-20098730; PubMed-10631266;
Harder P.A., Silverstein R.A., Meier I.;
"Conservation of matrix attachment region-binding filament-like
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9M7J4;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2224
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                                                                                                              Nuclear protein; DNA-binding; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                             tein 1 among higher plants.";
nt Physiol. 122:225-234(2000),
FUNCTION: BINDS DNA. INTERACTS WITH CHROMATIN VIA MATRIX
ATTACHMENT REGIONS (MARS). LIKELY TO PARTICIPATE IN NUCLEAR
ARCHITECTURE BY CONNECTING CHROMATIN WITH THE NUCLEAR MATRIX
POTENTIALLY WITH THE NUCLEAR ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR MATRIX (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTQEKLRKALEQQIKELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NASISAAKRK----LESELQTLHSDLDELLNEAKNSEEKAKKAMYDAARLADELRAEQDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEQEENKVLRAQL---ELSQVRQEIDRRIQEKEEEFENTRKNHQRALDSMQASLEAEAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQSADKEIMSLKKKLTMLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAEALRMKKKLEADINELEIALDHANKANAEAQKNIKRYQQQLKDIQTALEEEQRARDDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKM
                                                                                                                             AF131231; AAF36519.1; -
1 Similarity 23.1 55; Conservative
                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EQLGISERRANALQNELEESRTLLEQADRGRRQAEQ-----
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                                                                                                                                                                      requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
filament-like protein 1-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                  685
                                                                     24
82160
             14.2%;
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                                                                      MW.
 46;
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             Score 151;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 152;
Pred. No. 0.
                                                                COILED COIL (POTENTIAL).
POLY-SER.
BEB00B96103EA586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
 Mismatches
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             DB
.11;
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99;
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                          Length 722;
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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38;
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Gaps
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                                                                                                                                                                                                                                                         AL J. Moll. Biol. 205:603-613(1989).

AL J. Moll. Biol. 205:603-613(1989).

C -i- FUNCTION: MUSCLE CONTRACTION.

C -i- SUBUNIT: MUSCLE CONTRACTION.

C -i- SUBUNIT: MUSCLE CONTRACTION.

C -i- SUBUNIT: MUSCLE CONTRACTION.

C -i- SUBCELLULAR LOCATION: IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

C -i- AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

C -i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

C -i- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

C -i- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

C -i- PIM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY

C C ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

C -I- MISCELLANEOUS: EACH MYOSIN HEAVY MEROMYOSIN ATPASE ACTIVITY IN TO 1 LIGHT MEROMYOSIN (LAM) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER BE

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED

CC SUBFRAGMENT (S2).

C -I- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C SUBFRAGMENTS: THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.

CC -I- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989
01-OCT-1989
16-OCT-2001
                                  EMBL; X08067; CAA30856.1;
PIR; S02771; S02771.
HSSP; P08799; 1LVK.
                                                                                                            entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                     modified and this statement
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dibb N.J., Maruyama I.N., Krause M., Karn J.; "Sequence analysis of the complete Caenorhabditis elegans heavy chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYO-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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(Rel. 12, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
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                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QAQEEAGRLRSKMKTMEQIEL
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                                                                                                                                                                                                                              a collaboration
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                                                                                                                                                                                                            outstation
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Myosin_N.

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RESULT 24

KUCR_MOUSE

ID KUCR_MOUSE

AC P70194;

DT 01-NOV-1997

DT 16-OCT-2001

DE KUPFFER Cell

GN KCLR

OS Mus musculus

OC Mammalia;

NO MOBILTAXID=1

RN [1]

RP SEQUENCE FR

RC STRAIN=BALB,

RA TAKCZAWA R.

RL SUBMITTE (1)

CC -!- FUNCTIOL

CC -!- SIMILAR

CC -!- SIMILAR
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Best Local S
Matches 64
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Pfam; PF00063; myosin_head; 1.
Pfam; PF002736; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM000142; MYSC; 1.
                                                                                                                                                                                                  01-NOV-1997
01-NOV-1997
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
DOMAIN
DOMAIN
            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
MOD_RES
MOD_RES
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DOMAIN
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                               Mus musculus
                                                                                                                                                                                         Kupffer cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                 EEELEAERNSRQKSDRSRSEAERELEELTERL 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVIIDT------LRDTLEE---RNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQD 92
                                                                                                                                                                                                                                                                                                                                                              LKVAQENIDEITKQKHDVETTLKRKEEDLHHTNAKLAENNSIIAKLQRLIKELTARNAEL 1131
                                                                                                                                                                                                                                                                                                                                                                                     LKKEYENLKEARKASGEVADKLRK----DLFSSR-----SKLQTVYSEL-----
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                                                                                                                                                                                                                                                                                                                                       -DQAKLELKSAQKDLQS---ADKEIMSLKKKL
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ALKYLATION (SH-2) (PO)
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                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                       QLLGSHLEDVNADILQTKDVLKESGALALETQALRSSLEVASADIHSLRGDLEKANAMTS 197
TSSLNSRIEVVNGQMKDASRELQTLRRDL----SDVSALKSNVQMLQ
                                                                  EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL-KEARKASGEVADK----
                    S---RSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                             NISAQIQTV---RDGMERAGEKMNSLKKELETLTAQTQKANGHLEQTDAQIQGLKAELKS
                                                                                                               TLKKQMKY------LEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLP
                                                                                                                                                              EFLKNELDNVRAQLSQ~KDKEKRDSQVIIDT--LRDTLEERNATVVSLQQALGKAEMLCS
                                                                                          QTRGLLKSSTENTSAELHVLGRGLEEAQSE---IQALRGSLQSANDLSSQTQGFLQHSMD
                                                                                                                                                                                     Similarity 26.0
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C_TYPE_LECTIN_2; 1.
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
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STRAIN-K1
                                                                            DNA double-strand RAD50 OR APE0110.
                                                                                                                                                AERPE
 MEDLINE=99310339; PubMed=10382966;
                                                Aeropyrum
                                                          Archaea; Crenarchaeota;
                                                                   Aeropyrum pernix
                                                                                                                                      RA50_AERPE
                                      NCBI_TaxID=56636;
                   FROM N.A
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16-OCT-2001 (Rel. 40, Create 16-OCT-2001 (Rel. 40, Last s 16-OCT-2001 (Rel. 40, Last s Probable DNA double-strand b RA550 OR AQ_1006.
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DNA Res. 6:83-101(1999).

DNA Res. 6:83-101(1999).

The rad50/mrell complex possesses single-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity and ATP-dependent double-strand-specific exonuclease activity and ATP-dependent control of mrell by unwinding and/or repositioning The Complex per and a transfer to the control of mrell by unwinding and/or repositioning The Complex per and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding and a transfer to the control of mrell by unwinding the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003439; ABC_transportr. InterPro; IPR001687; ATP_GTP_A. InterPro; IPR003405; SMC_C. Pfam; PF02483; SMC_C; 1.
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                          Aquifex aeolicus
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Best Local
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EMBL; AE000718; AAC07092.1; ...

InterPro; IPR003439; ABC_transportr.

InterPro; IPR003439; ABC_transportr.

DNA repair; Hydrolase; ATP-binding; Coiled coil;

DNA repair; Hydrolase; ATP-binding; Coiled coil;

DNA repair; Hydrolase; ATP-binding; Coiled coil;

ONA repair; Hydrolase;
                                                                                                                                                                               MYH1_HUMAN STANDARD; PRT; 1939 AA. P12882; Q9Y622; 01-OCT-1989 (Rel. 12, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Myosin heavy chain, skeletal muscle, adult 1 IIx/d) (MyHC-IIx/d).
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-I- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity.

Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE FROM
                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Forms a complex with mrel1 (By SIMILARITY: BELONGS TO THE SMC FAMILY. F
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                                                                                                                               (Human)
                                                                         Chordata;
Primates;
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26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 149; DB Pred. No. 0.2;
                                                                         Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLED COIL (POTENTIAL).
9B0F2BF51ADD1151 CRC64;
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                                                                            Hominidae;
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RAD50 SUBFAMILY.
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RL NUCLEIC ACIDS Res. 14:2951-2969(1986).

RL NUCLEIC ACIDS RES. 14:2951-2969(1986).

CC -!- FUNCTION: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MLC) 2

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CC -- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY

CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

CC -- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC SUBERAGMENT (S2).

CC -- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

CC -- SIMILARITY: CONTAINS 1 DOMAIN.
                                                                                                                                                                                                                                                                                                          Pfam; PF00063; myosin_head; 1.
Pfam; PF01576; Myosin_tail; 2.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000122; MYSG; 1.
                                                            CONFLICT
CONFLICT
                                                                                                                     MOD_RES
MOD_RES
MOD_RES
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DOMAIN
                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                Myosin; Muscle protein; Coiled co
Calmodulin-binding; ATP-binding;
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                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99318869;
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048;
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InterPro; IPR001609; myosin_head.
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L.A.;
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METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
A -> T (IN REF. 2).
Q -> L (IN REF. 2).
G -> V (IN REF. 2).
A -> T (IN REF. 2).
TESG -> ONOV (IN REF. 2).
VS -> ET (IN REF. 2).
R -> T (IN REF. 2).
R -> T (IN REF. 2).
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IQ.
COILED COIL (POTI
                                                                                                                                                              ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
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Matches 52
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029230;
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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"The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- FUNCTION: Involved in DNA double-strand break renair (neps)
                                                                                                                                                                                                                                                                     Kienk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D. Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Richardson D.L., Ouackenbush J., Lee N.H., Sutton G.G., Gill Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterbac Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                       <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Archaea; Euryarchaeota;
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                                                                                                   rad50/mre11 complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mre11 by unwinding
                       SUBUNIT: Forms a complex with mrell (By SIMILARITY: BELONGS TO THE SMC FAMILY. )
                                                                similarity)
                                                                                  and/or repositioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KR----QLEEEIKAKSALAHALQSSRHDCDLLREQYEEEQEAKAELQRAMSKANSEVAQW 1375
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40, Last sequence update)
40, Last annotation update)
break repair rad50 ATPase.
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                                                                                  ic exonuclease activity l of mrell by unwinding mrell active site (By
                       / similarity).
RAD50 SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                             J.D.,
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                                                                                                                                                                                                                                                                                                                                          Zhou L.,
ick T.,
                                                                                                                                                                                                                                                                                                                                                                                 8.
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P33176;
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Kinesin heavy chain (KIF5B OR KNS1 OR KNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001238; RecF.
InterPro; IPR002017; Spectrin.
Pfam; PF00470; RecF; 1.
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
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                                        MEDLINE=96195066;
Kull F.J., Sablin
                                                                                                                           interaction of the COOH-terminal domain
in transfected CV-1 cells.";
J. Cell Biol. 117:1263-1275(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                      "Crystal structure
                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
                                                                                                                                                                                          McCaffrey G., Vale R.D.;
"Cloning and expression of a human kinesin heavy
                                                                                                                                                                                                                                     Navone F.,
                                                                                                                                                                                                                                                         MEDLINE=92299683;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606
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148
886 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                        PubMed=8606779;
E.P., Lau R., F
                                                                                                                                                                                                                                   PubMed=1607388;
J., Hom-Booher
                    of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728
103633
                                                                                                                                                                                                                                                                                                                                                                   Primates;
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Lau R., riche kinesin motor
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COILED COIL (POTENTIAL)
W; D35641D499AA8B58 CRC
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; I Catarrhini; Hominidae;
               Fletterick R.J., Vale R.I
in motor domain reveals a
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                                                                                                                                                                                                                                   Sparks L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     963
                                                                                   OF 1-349
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                                                                                                                                                                  eavy chain gene:
cytoplasmic mic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                   Bernstein
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                                                                                                                                                                                                                                                                                                                                                                   Homo
                                        R.D.;
                    structural
                                                                                                                                                                      microtubules
                                                                                                                                                                                                                                   H.D.
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Best Local
                                                                                                                                                                                                                                                 Matches
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Neuron 12:1059-1072(1994).

-i- function: Kinesin is a microtubule-associated force-
-i- function: Kinesin is a microtubule-associated force-
-i- protein that may play a role in organelle transport-
-i- Subunit: Oligomer Composed of two heavy chains and '
                                                                                                                                                                                                                                                                                                                         NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Microtubules; ATP-binding; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity to myosin.";
Nature 380:550-555(1996).
                                                                                                                                                                                                                                                                                                                                                        Motor protein; Microtubules; ATP-binding; C
DOMAIN 1 256
MINESTN-MOTOR.
DOMAIN 329 914 COLLED COIL.
DOMAIN 915 963 GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94242426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00225; kinesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Niclas J., Navone F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
605
                              112
                                                                                                                       485
                                                                                                                                                                                    425
                                                           545
                                                                                        73
                                                                                                                                                     37
                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAINS.
SUBCELLULAR LOCATION: UNIFORMLY DISTANCE.
AND THE PROCESSES IN THE NEURONS.
TISSUE SPECIFICITY: FOUND IN NEWBORN AND ADULT
SOLFEN. HEART, LUNG AND SCIATIC NERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIDNEY, SPLEEN, HEART, LUNG AND SCIATIC NERVE.

DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINE MOTOR ACTIVITY OF
TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL
ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN
DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAIN)
VESICLES AND MEMBRANOUS ORGANELLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: OLIGOMER CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A41919; A41919.
1BG2; 14-OCT-98
VKRCKQLESTQTESNKKMEENEKELAACQLRISQHEAKIKSLTEYLQNVEQKKRQLEESV
                                                                                                                                                                                    IAKLYKQLDDKDEEINQQSQLVEKLKTQMLDQEELLASTRRDQDNMQAELNRLQAENDAS
                                                                                                                                                                                                               INKLFFDLAQEEENV - - - -
                                                                                                                       KEEVKEVLQALEELAVNYDQKSQEVEDKTKEYELLSDELNQKSATLASIDAELQKLKEMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X65873; CAA46703.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00129; KISC;
                                                                                                                                                                                                                                               . Similarity 67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR00380; KINESINHEAVY.
                            -EQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001752; kinesin.
                                                                                                                                                                                                                                                                                                                           963 /
                                                                                        AEMLCSTLK-----
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                            ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=7514426;
                                                                                                                                                                                                                                                                                                                            109685
                                                                                                                                                                                                                                                            13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hom-Booher N., Vale
                                                                                                                                       QKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIFORMLY DISTRIBUTED BETWEEN THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -Booher N., Vale R.D.;
of a conventional kinesin motor expressed
                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                               55;
                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                         ATP (BY SIMILARITY)
i; AlfE5760C3250C8B
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                    148.5; E
                                                                                        -KQMKYLEQQQDETKQAQEEAGRLRSKMKTM
                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                               94;
                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORCE-PRODUCING
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BRAIN, LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                      3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OWI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ωı
                                                                                                                                                                                                                                               95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BODY
                              167
                                                                                                                                                                                    48
                                                                                                                       544
                                                           604
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RESULT
MYH7_ME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYH7_MESAU STANUARL,
P13540; Q60540;
O1-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _MESAU
                                                                                                                                                         EMBL; L12104; AAA62313.1; -.
EMBL; X07273; CAA30256.1; -.
PIR; A28298; A28298.
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 962-1935 FROM N.A MEDLINE-88247788; PubMed-3380; Jandreski M.A., Sole M.J., Lit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang R., Sole M.J., Cukerman E., Liew C.-C.; "Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain gene from Syrian hamster."; J. Mol. Cell. Cardiol. 26:1155-1165(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=F1B; TISSUE=Liver; MEDLINE=95115033; PubMed=7815459;
                                                  Piam;
                                                                                InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002028; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jandreski M.A., Sole M.J., Liew C.-C., "Sequence of cDNA encoding the Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
i; PF00612; IQ; 2.
a; PF00063; myosin_head; 1.
n; PF02736; Myosin_N; 1.
n; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
REAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
SUBUNIT: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 1 HEPTAPEPTIDES,
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN (CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFRAGMENT (S2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: MUSCLE CONTRACTION
                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKLRKDLFSSR------SKLQTVYSELDQA----KLELKSAQKDLQSADKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=3380703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia; Sciurognathi; Muridae;
                                                                              myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hamster cardiac beta-myosin
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                                                                                                                                                                                                                               MYSS_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                   MYSS_CHICK STANDARD; PRT; 1938 AA.

P13538; 013228;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, adult.
Gallus gallus (Chicken).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; ATP-binding; Methylation; Alkylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
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                                                                                                                                                                                                                                                                                                                                            167
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                                                                                                                                                                                                                                                                                                      LSKANSEVAQWRTKYETDAIQRTEELEEAKKKL--AQR-LQDAEEAVEAVNAKCSSLE
                                                                                                                                                                                                                                                                                                                                            ADKLRKDLFSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KANLEKMCRTLEDQMNEHRSKAEETQRSVNDLTSQRAKLQTENGELSRQLDEKEALI-SQ 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKT------MEQIELLLQSQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAEFQKMRRDLEEATLQHEAT 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTIINKLFFDLAQEEENVLDR-------EFLK-----
                                                                                                                                                                                                                                                                                                                                                                                 LTRGKLTYTQQLEDLKRQLEEEVKAKNTLAHALQSARHDCDLLREQYEEETEAKAELQCV 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDDVTSNMEQ------IIKA 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              986
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LATTON (SH.

SE (IN REF. 2).

E (IN REF. 2).

E -> TE (IN REF. 2).

E -> Q (IN REF. 2).

DLQAEED -> ALEARKT (IN REF. 2).

DL -> Y (IN REF. 2).

L -> V (IN REF. 2).

1217 E -> D (IN REF. 2).

1217 E -> D (IN REF. 2).

1271 D -> N (IN REF. 2).

1271 T -> A (IN REF. 2).

1271 T -> A (IN REF. 2).

1272 T -> A (IN REF. 2).

1274 C -> R (IN P.

1 -> V (IN P.

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ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
D -> E (IN REF. 2).
T -> TE (IN REF. 2).
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Archosauria; Aves; Neognathae;

Galliformes;

Phasianidae;

Euteleostomi;

Phasianinae;

NCBI_TaxID=9031

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TISSUE-Pectoralis muscle;
MEDINE-92041770; PubMed-1939030;
Maita T., Yajime E., Nagata S., Miyanishi T., Nakayama S., Mai
"The primary structure of skeletal muscle myosin heavy chain:
Sequence of the rod, and the complete 1,938-residue sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE C. TISSUB-Pectoralis muscle;
MEDLINE-92041767; PubMed-1939027;
MEDLINE-92041767; PubMed-1939027;
Maita T., Matsuda G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chao T.H., Bandman E., Moore L.; "Cloning, nucleotide sequence and cDNA encoding the myosin heavy chamajor muscle.";
Moriarity Young R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                           Maita T., Hayashida M., Tanioka Y., Komine Y., "The primary structure of the myosin head."; Proc. Natl. Acad. Sci. U.S.A. 84:416-420(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maita T., Miyanishi T., Matsuzono K., Tanioka Y., Matsuda G.; "The primary structure of skeletal muscle myosin heavy chain: "The primary structure of skeletal muscle myosin heavy chain: Sequence of the 22 kDa fragment and the alignment of the 23 kDa, and 22 kDa fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The
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Biol. Chem. Hoppe-Seyle
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MEDLINE=90121764; Pul
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MEDLINE=92041769; PubMed=1939029;
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STRAIN=WHITE
                              SEQUENCE OF 1857-1938 FROM N.A. MEDLINE=87217964; PubMed=3034534;
                                                                                                                                 Watanabe
                                                                                                                                                 MEDLINE=89228549;
                                                                                                                                                                  SEQUENCE OF
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                                                                                                                                                                                                                "Amino-acid
skeletal mus
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                                                                                                                                                                                                                                                                MEDLINE=89374803;
                                                                                                                                                                                                                                                                               [8]
SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                  "Complete amino-acid sequence of skeletal muscle myosin.";
                                                                                                                                                                                                                                                                                                                                                                Watanabe B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87092420;
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This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBIT the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic clones encoding chicken myosin heavy-chain genes."; DNA 6:91-99(1987).
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SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SUBUCELLULAR LOCATION: Thick filaments of the myofibrils. DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOW CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPED CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        U87231; AAB47555.1; M16557; AAA48970.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
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R., Benning M.M.,
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Pubmed=8316857;
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Pfam; PF00063; myosin_head;
Pfam; PF02736; Myosin_tail;
Pfam; PF01576; Myosin_tail;
ProDom; PD000355; myosin_hea PIR; PIR; PIR; PIR; InterPro; IPR004009; InterPro; IPR002928; InterPro; IPR001609; DOMAIN Calmodulin-binding; Multigene INIT_MET 0 0 Myosin; Muscle PROSITE; DOMAIN DOMAIN DOMAIN ATP-binding; InterPro; PX0050; A26821; S02082; S04501; S05515; 2MYS; SM00015; IQ; 1 SM00242; MYSC; PS50096; IQ; IPR000048; IQ.
IPR004009; Myosin_N.
IPR002928; Myosin_ta 11-JAN-97 783 838 841 179 179 657 759 S04501. S05515. A26821 S02082 Methylation; Alkylation; protein; Coiled coil; Thick filament; /osin_tail; 1.
myosin_head; 782 812 840 1938 186 679 773 1 1 130 551 myosin_head. _tail MYOSIN IQ. ATP (POTENTIAL). ACTIN-BINDING. ACTIN-BINDING. HINGE. COIL (POTENTIAL). METHYLATION METHYLATION ACETYLATION METHYLATION family; HEAD-LIKE 3D-structure Phosphorylation; (TRI-). (TRI-). (MONO-). (MONO-). Actin-binding; n; Acetylation;

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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle (Cellular myosin MYH).
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                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Intestinal epithelium;
MEDLINE=90046668: PubMed=2813355;
Shohet R.V., Conti M.A., Kawamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of the cDNA encoding the myosin heavy chain cellular myosin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adelstein R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                       CAPPING.

SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2),

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPAGED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILES.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILES.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILES.
                                                                                                                                                                                                                                                                                                                                                                                 C. Natl. Acad. Sci. U.S.A. 86:7726-7730(1989)
FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A 1
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AN
                                                                                                                                SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD SIMILARITY: CONTAINS 1 IQ DOMAIN.
                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTKYETDAIQRTEELEEAKKKLAQ---RLQDAEEHVEAVNAKCASLEKTKQRLQ 1424
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Neognathae; Galliformes; Phasianidae;
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> V (IN REF. 10).
-> FH (IN REF. 10).
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SQ144444444
SEQUENCE FROM N.A.

MEDLINE-83273600; PubMed-6576

Karn J., Brenner S., Barnett

"Protein structural domains i

myosin heavy chain gene are n

Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PrODom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                           21-JUL-1986 (Rel. C
21-JUL-1986 (Rel. C
16-OCT-2001 (Rel. 4
                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000048; IO.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                     Myosin heavy chain UNC-54 OR MYO-4.
                                                                                                                                                                                                                                    MYSB_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A33977; A33977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1665 LAQAKENEKKLKSMEAEMIQLQEELAAAERAKRQAQQERDELADEIANSSGKGALAMEEK
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1 B (MHC B).
                                                   PubMed=6576334;
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22.7%;
                                        Barnett
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mains in the Caenorhabditis elegans e are not separated by introns."; U.S.A. 80:4253-4257(1983).
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ATP (POTENTIAL).
ACTIN-BINDING.
ALKYLATION (SH-1) (POTENTIALYLATION (SH-2) (POTENTIALYLATION (SH-2))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 148.5; D
Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                      1966
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                                                                                                                        Rhabditida;
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InterPro; IPR002928; Myosin_tail.
InterPro; IPR001699; myosin_head.
Pfam; PP00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genes sup-7 X and sup-5 III of C. elegans nonsense mutations via altered transfer RNA."; Cell 33:575-583(1983).
                                           MOD_RES
MOD_RES
MOD_RES
                                                                                                                  DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 EMBL; J01050; AAA28124.1;
EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
HSSP; P08799; IMND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 850-1966 FROM MEDLINE=82272395; PubMed=""" A n Karn J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Periodic charge distributions in the myosin match cross-bridge spacings in muscle.";
                                                                                     DOMAIN
                                                                                                                                                                                                   Myosin; Muscie procein; co
                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                    DOMAIN
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                                                                                                                                                                                                                                  SMART; SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McLachlan A.D., Karn J.;
                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004009; Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBERAGMENT (S2).

MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C.ELEGANS.

MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE BODY WALL THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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1165
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PubMed=6571695;
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PubMed=7202124;
   225125
                                                                                                                                                                                                                   Coiled coil;
                                                                                                                                                                                                         Alkylation;
   ž
                ALKYLATION
E -> R (IN
I -> L (IN
                                                                                    ATP (BY SIMILAR ACTIN-BINDING. ACTIN-BINDING.
                                                                                                                                                      ed coil; Thick filament; Actin-binding; cylation; Multigene family.

MYOSIN HEAD-LIKE.

COILED COIL (POTENTIAL).

ALPHA-HELICAL TAILPIECE (S2).
                                       METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                               LIGHT MEROMYOSIN (LMM)
> R (IN REF. 2).
> L (IN REF. 2).
B66F0BB2FE27B67F CRC64;
                                                                                                                (BY SIMILARITY).
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Best Local
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PIR; B36014; B36014
HSSP; P08799; 1MMD
                                                                                                                                                           modified and this statement entities requires a license
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"Complete sequence of the Drosophila nonmuscle myosin
transcript: conserved sequences in the myosin tail and
splicing in the 5' untranslated sequence.";
Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
CBI_TaxID=7227;
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                                                         FlyBase;
                                                                                                                                                or send
                                                                                                                                                                                           use
                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                               SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
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16-OCT-2001
                            InterPro;
                                             InterPro;
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                                                                                                                                                                                                                       between
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                                                                                                                                                                                                                                                                                            FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS. ALTERNATIVE PRODUCTS: 2 ISOFONKS; A LONG FORM (SHOWN HERE) & SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                              IPR004009;
                IPR002928;
                                                                                                                                                email to license@isb-sib.ch)
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Last annotation update)
(Myosin
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B36014.
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; IQ.
; Myosin_N.
; Myosin_tail.
; myosin_head.
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21.3%;
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Best Local S
Matches 57
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                  Q02224;
01-JUL-1993
01-JUL-1993
30-MAY-2000
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PTCDOMS, PD000355; MYOSIn_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                              MEDLINE-93024922; PubMed Yen T.J., Li G., Schaar
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Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
CHARACTERIZATION
                                                                             "CENP-E
                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTIINKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKR--DSQVI-----ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RARSELQEK---CTKLQQEAENITNQLEEAELKASAAVKSASNMESQLTEAQQLLEEETR 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLRDTLEERNATVVSLQQ------ALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTVLEKAKGTLEAENAD------LATELRSVNSSRQENDRRRKQAESQTAELQVKLAETE 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKLGLSSKLRQIESEKEALQEQLEEDDEAKRNY - - - ERKLAEVTTQMQEIKKKAEEDADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKELEEGKKRLNKDIEALERQVKELIAQNDRLDKSKKIQSELEDATIELEAQRTKVLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00063;
                                       359:536-539(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 23.7
57; Conservative
                                                                  is a putative kinetochore motor that accumulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing;
                                                                                                                                                                                                                                                                               (Rel. 26, Rel. 26, Rel. 36, Rel. 39, Protein E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830
886
225
250
682
705
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
A
                                                                                                  PubMed=1406971;
Schaar B.T., Szilak I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859
2017
232
260
694
727
758
2017
1970
                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.8%;
23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232016
                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                  (CENP-E
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25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN BINDING.
REACTIVE SULPHYDRYL/ACTIN-BINDING.
LIGHT MEROMYOSIN (LMM).
ALPHA-HELICAL TAILDIECE (LMM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 147.5; | Pred. No. 0.49 | Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR TAILPIECE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQ.
COILED COIL (POTENTIAL)
                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73E3CB02BA8F2528
                                                                                                                                                                                                                                                                                                                                                                                    2663
                                                                                                Cleveland D.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102;
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                                                                             just
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                                                                               before
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Matches
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NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z15005; CAA78727.1; -. PIR; S28261; S28261. HSSP, P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by anc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E revinteractions with the kinetochore proteins CENP-F and hBUBRI.";

J. Cell Biol. 143:49-63(1998).

-i- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2:

OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.
1810
                                                         1750
                                                                                                                    1693
                                                                                                                                                                              1638
                                                                                                                                                                                                                                                                                                                                                                       Motor process: Centromere.
Cell cycle; Centromere.
335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wils "Mitotic HeLa cells contain a CENP-E-associated minus microtubule motor.";
                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P17119
MIM; 117143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                    Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00380; KINESINHEAVY. SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98437347; PubMed=9763420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95196755; PubMed=7889940;
                           173
                                                                                     124
                                                                                                                                               72
                                                                                                                                                                                                        13 QEEENVLDREFLKNELDNVRAQLSQKDKEK-RDSQVIIDTLRDTLEERNATVVSLQQALG 71
                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: INTERACTS WITH CENP-F AND BUBRI KINASE.
SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE,
QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY
                          DLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADK---EIMSLKKKL
                                                      SVE---ETLKVERDQLKENLRETITRDLEKQEELKIVHMHLKEHQETIDKLRGIVSEKTN
                                                                                                                                             KAEMLCSTLKKQMKYLEQQQDET----KQAQEEAG----RLRSKMKTMEQIELLLQSQLP 123
                                                                                                                                                                            ETQEKMCEIEHLKEQFETQKLNLENIETENIRLTQI----LHENLEEMR-SVTKERDDLR 1692
DLENSNAKLQEKIQELKANEHQLITLKKDVNETQKKVSEMEQLKKQI 1856
                                                                                                                                                                                                                                       . Similarity 57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14:918-926(1995).
                                                                                                                                                                                                                                                                                                                                           2472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            336
                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                            2471
2663
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312087
                                                                                                                                                                                                                                                     13.8%;
25.1%;
                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                             KINESIN-MOTOR.
COILED COIL (POTENTIAL)
GLOBULAR (POTENTIAL).
ATP (BY SIMILARITY).
MW; CEFC13880C8C8CBB CI
                                                                                                                                                                                                                                                                                                                ATP
                                                                                                                                                                                                                                                     Score 147.5;
Pred. No. 0.
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                     No. 0.65;
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                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                CRC64;
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                          216
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                                                                                                                                                                                                                                       Gaps
                                                                                     172
                                                                                                                    1749
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RESULT 36
Y373_BOVIN
ID Y373_BOVIN

STANDARD;

PRT;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                      P58302;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
DNA double-strand break repair
RAD50 OR TVG0235331. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF176816; AAF00990.1;
Hypothetical protein; Coiled
DOMAIN 37 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jovov B., Ripoll P.J., Benos D.J.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
SEQUENCE FROM N.A
STRAIN=GSS1 / DSM
MEDLINE=20570466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Trachea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIAA0373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9TU23;
16-OCT-2001
                                                                 Thermoplasma
                                                                            Archaea; Euryarchaeota; Thermoplasmales;
                                                                                         Thermoplasma volcanium.
                                                                                                                                                                                    RA50_THEVO
                                                                                                                                                                                                  THEVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EENVLDREFLKNEL------DNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVV
                                                                                                                                                                                                                                                 TTTMRNLVERLKSQLALKEKQQKALSRALLELRAEMT
                                                                                                                                                                                                                                                                                                     KIKEFENMKLRLQENHADEVKKIKAEVED-LRCLLVQSQKESQSLKSELQTQKEANSRAP
                                                                                                                                                                                                                                                                                                                                 --KEYENLK--
                                                                                                                                                                                                                                                                                                                                                                                                             NMQARLNQKE---EVLKKYQHLLEKAREEQREIVKKHEEELHTLHRKLELQADNSLSKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                     SLQQALGKAEMLCSTLKKQMKYLEQQQDE----TKQAQEEAGRLRSKMKTMEQ---
                                                                                                                                                                                                                                                                                                                                                         ETAWDLIKQSPTPVPTNKHFIRLAEMEQTVAEQDDSLSSLVIKLKQVSQDLERQKEITEL
                                                                                                                                                                                                                                                                                                                                                                                   ---IELLLQS--QLPEVEEMIRDMGVGQSAVEQ---LAVYCVSLK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1453 AA;
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(Rel. 40,
(Rel. 40,
protein K
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                                                                                                                                                                                                                                                                            -DQAKLELKSAQKDLQSADKEIMSLKKKLT
                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4299 / JCM 9571;
PubMed=11121031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Created)
, Last sequence update)
, Last annotation updat
KIAA0373.
                                                                                                                                                                                                                                                                                                                               ---EARKASGEVADKLRKDLFSSRSKLQTVYSEL
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                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147; DB
Pred. No. 0.37
49; Mismatches
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                                                                                                                    ATPase
                                                                                                                                                                                    895
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                                                                           Thermoplasmaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622
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RESULT 38
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Best Local
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Kawashima-Chya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
"Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
-!- FUNCTION: Involved in DNA double-strand break repair (DSBR). Tl
rad50/mrell complex possesses single-strand endonuclease activity.
and ATP-dependent double-strand-specific exonuclease activity.
Rad50 provides an ATP-dependent control of mrell by unwinding
and/or repositioning DNA ends into the mrell active site (By
Myosin heavy cuma..., ...
Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Leporidae; Oryctola;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
-!- SUBUNIT: Forms a con
-!- SIMILARITY: BELONGS
                                                      21-JUL-1986 (Rel. 01, Created)
01-JAN.1990 (Rel. 13, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
Myosin heavy chain, skeletal muscle ()
                                                                       21-JUL-1986 (Rel.
01-JAN-1990 (Rel.
15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                    MYSS_RABIT
P02562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP_BIND 30 37 ATP (BY SIMILARITY).
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TY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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103223 MW;
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22.8%;
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Pred. No. 0.24;
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COILED COIL (POTENTIAL).
4A47DA9287E82D3A CRC64;
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on update)
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              Oryctolagus
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PIR; A05280; A05280.
PIR; S00084; S00084.
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Myosin; Muscle protein; Coi
ATP-binding; Multigene fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05958; CAA29391.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maeda K., Sczakiel G., Wittinghofer A.;
"Characterization of cDNA coding for the complete light meromyosin portion of a rabbit fast skeletal muscle myosin heavy chain.";
Eur. J. Biochem. 167:97-102(1987).
-!- FUNCTION: MUSCLE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                                                                   NON_CONS
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Maeda K., Sczakiel G., Wittingho!
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The amino acid sequence and
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"The amino acid sequence
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                                      24 LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQ 83
                                                                                                                     Local
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HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MEC).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILES OF COILS.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
SPLIT FURTHER INTO 2 GLOBULAR SUBERRAGMENTS (S1) AND 1 ROD-SHAPED
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SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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P50532;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                 MITOTIC CHROMOSOMES.
SUBBUNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER.
SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COLLED-COLL REGIONS
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COLLED-COLL REGIONS
                                                                                                                                                                                                                                                                                                                                                                          FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS SIMILARITY: BELONGS TO THE SMC FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLA 143
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IPR003405;
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ed coil; Nuclear protein.
ATP (POTENTIAL).
COILED COIL (POTENTIAL).
POLY-PRO.
POLY-GLY.
POLY-GLY.
POLY-GLY.
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ALA/ASP-RICH (DA-BOX).
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Query Match Best Local Similarity

13.7%; 21.2%;

Score 146; DB 1; Pred. No. 0.38;

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Matches
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MYH3_HUMAN STANDARD,
P11055; Q15492;
O1-JUL-1989 (Rel. 11, Created)
O1-JUL-1989 (Rel. 11, Last sequence update
16-CCT-2001 (Rel. 40, Last annotation upda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HUMAN
MEDLINE-89366648; PubMed-2771643;
Karsch-Mizrachi I., Travis M., Blau H., Leinwand L.A.;
"Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin heavy chain gene.";
nucleic Acids Res. 17:6167-6179(1989).
-!- FUNCTION: MUSCLE CONTRACTION.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF HEAVY CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                   Eller M.S., Stedman n..., Eller M.S., Stedman n..., Rubinstein N.A., Kelly A.M., Rubinstein N.A., sequence of full
                                                                                                                                       myosin
                                                                                                                                                                                     TISSUE=Skeletal muscle; MEDLINE=90235862; PubMed=1691980;
                                                                                                                                                                                                                                    specific transcription of t
FEBS Lett. 256:21-28(1989).
                                                                                                                                                                                                                                                conservation of the myosin rod, chromosomal locus
specific transcription of the gene.";
                                                                                                                                                                                                                                                                       Eller M.S., Stedman H.H., Sylvester J.E., Raychowdhury M.K., Rubinstein N.A., Kelly "Human embryonic myosin heavy chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                               Arnold H.H.;
"Identification of three
                                                                                                                                                                           Bober
                                                                                                                                                                                                             SEQUENCE OF 856-1940 FROM N.A.
                                                                                                                                                                                                                                                                                                             MEDLINE=90033298; PubMed=2806546;
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 774-1940 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89263803; PubMed=2726495;
Eller M.S., Stedman H.H., Sylvest
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                          Biochem. 189:55-65(1990)
                                                                                                                                                                                                                                                                                                                                                  Acids Res. 17:3591-3592(1989).
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Primates;
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.M., Sarkar !
full length !
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Catarrhini;
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y A.M., Sarkar S
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                                                                                     Local
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                                                LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQ
                         LGEQIDNLQRVKQKLEKEKSEFKLEIDDLSSSME-----SVSKSKANLEKICRTLEDQ
                                                                          52; Conser
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TO PER CONTROL OF STREET O

Conservative

50;

Pred. No. 0.5: 0; Mismatches

85;

Indels

36;

7;

83

-QEEAGRLRSKMKTMEQIELLL---

-QSQLPEVEEM 128

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use by non-profit institutions as lo modified and this statement is not rementitles requires a license agreement or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copy herween the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S04090; S
HSSP; P08799;
                                                                                                                                                                                                                                                                                                      Calmodulin-binding; ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                      Myosin; Muscle protein;
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 160720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001609; Pfam; PF00612; IQ; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.

MISCELLANEOUS: ACH MYOSIN HEAVY CHAIN CAN BE SCHIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DEVELOPMENTAL STAGE: ABUNDANTLY PRESENT IN FETAL SKELET/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND NOT PRESENT OR BARELY DETECTABLE MUSCLE.
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X13100; CAA31492.1;
X51593; CAA35942.1;
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                                                                                                                                                                                                                                                                                                                      Coiled coil;
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                                                           ALKYLATION (SH-1).
ALKYLATION (SH-2).
A -- G (IN REF. 3).
A -- G (IN REF. 1 AN SR -- PA (IN REF. 2).
RG -- OT (IN REF. 2).
SM: 43CA58C6A4BA1253
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Score 146;
Pred. No. 0
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COILED
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                                                                                                                                                                                                                                                                         MYOSIN HEAD-LIKE
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                                                                                                                                                                                                                                                                                                                      Thick filament; Actin-binding;
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